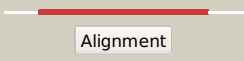

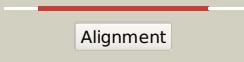

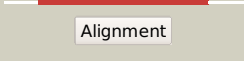

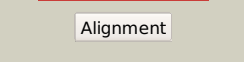

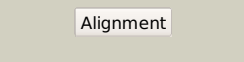

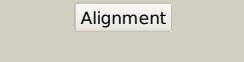

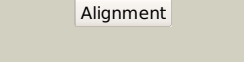

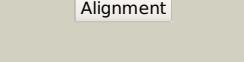

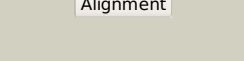

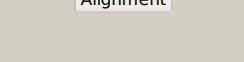

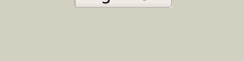

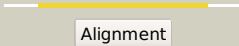
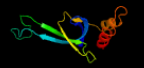
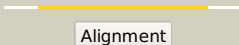

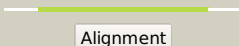

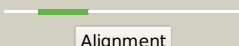

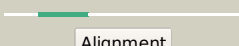
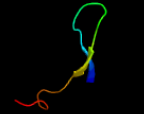
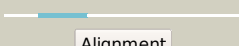

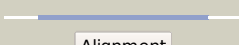


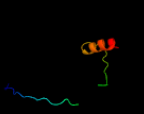




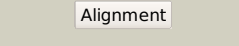
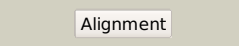


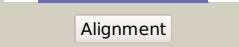



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1942c_(-)_2194651_2194980
Date	Mon Aug 5 13:25:03 BST 2019
Unique Job ID	509c8fe9b18667fb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ub4a_	 Alignment		100.0	29	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Kid/PemK
2	c5xe3B_	 Alignment		100.0	26	PDB header: hydrolase/antitoxin Chain: B: PDB Molecule: endoribonuclease mazf4; PDBTitle: endoribonuclease in complex with its cognate antitoxin from 2 mycobacterial species
3	c5wygC_	 Alignment		100.0	29	PDB header: hydrolase Chain: C: PDB Molecule: probable endoribonuclease mazf7; PDBTitle: the crystal structure of the apo form of mtb mazf
4	c4mzpC_	 Alignment		100.0	24	PDB header: hydrolase Chain: C: PDB Molecule: mazf mrna interferase; PDBTitle: mazf from s. aureus crystal form iii, c2221, 2.7 a
5	d1ne8a_	 Alignment		100.0	25	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Kid/PemK
6	c5hk3B_	 Alignment		100.0	27	PDB header: hydrolase/dna Chain: B: PDB Molecule: endoribonuclease mazf6; PDBTitle: crystal structure of m. tuberculosis mazf-mt3 t52d-f62d mutant in 2 complex with dna
7	d1m1fa_	 Alignment		99.9	28	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Kid/PemK
8	c5hizA_	 Alignment		99.9	25	PDB header: hydrolase/rna Chain: A: PDB Molecule: endoribonuclease mazf9; PDBTitle: structure of m. tuberculosis mazf-mt1 (rv2801c) in complex with rna
9	c5ccaA_	 Alignment		99.9	34	PDB header: hydrolase Chain: A: PDB Molecule: endoribonuclease mazf3; PDBTitle: crystal structure of mtb toxin
10	c3jrzA_	 Alignment		95.1	17	PDB header: toxin Chain: A: PDB Molecule: ccdb; PDBTitle: ccdbvfi-formii-ph5.6
11	d3vuba_	 Alignment		95.1	18	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: CcdB

12	c2l89A_	 Alignment		71.8	18	PDB header: protein binding Chain: A; PDB Molecule: pwpp domain-containing protein 1; PDBTitle: solution structure of pdp1 pwpp domain reveals its unique binding2 sites for methylated h4k20 and dna
13	d1h3za_	 Alignment		71.5	13	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: PWWP domain
14	c3llrA_	 Alignment		63.3	20	PDB header: transferase Chain: A; PDB Molecule: dna (cytosine-5)-methyltransferase 3a; PDBTitle: crystal structure of the pwpp domain of human dna (cytosine-5-)-2 methyltransferase 3 alpha
15	c5ikjA_	 Alignment		50.7	25	PDB header: transcription Chain: A; PDB Molecule: cryptic loci regulator 2; PDBTitle: structure of clr2 bound to the clr1 c-terminus
16	d2daqal	 Alignment		41.2	8	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: PWWP domain
17	c3bxpA_	 Alignment		35.2	15	PDB header: hydrolase Chain: A; PDB Molecule: putative lipase/esterase; PDBTitle: crystal structure of a putative carboxylesterase (lp_2923) from2 lactobacillus plantarum wcfs1 at 1.70 a resolution
18	c4ld6A_	 Alignment		23.5	16	PDB header: unknown function Chain: A; PDB Molecule: pwpp domain-containing protein 2b; PDBTitle: pwpp domain of human pwpp domain-containing protein 2b
19	c4bedA_	 Alignment		17.8	21	PDB header: oxygen transport Chain: A; PDB Molecule: hemocyanin klh1; PDBTitle: keyhole limpet hemocyanin (klh): 9a cryoem structure and molecular2 model of the klh1 didecamer reveal the interfaces and intricate3 topology of the 160 functional units
20	c4me8A_	 Alignment		16.9	18	PDB header: hydrolase Chain: A; PDB Molecule: signal peptidase i; PDBTitle: crystal structure of a signal peptidase i (ef3073) from enterococcus2 faecalis v583 at 2.27 a resolution
21	d1rz4a1	 Alignment	not modelled	14.1	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Eukaryotic translation initiation factor 3 subunit 12, eIF3k, C-terminal domain
22	c6g25A_	 Alignment	not modelled	13.7	19	PDB header: oncoprotein Chain: A; PDB Molecule: histone-lysine n-methyltransferase nsd3; PDBTitle: x-ray structure of nsd3-pwpp1 in complex with compound 4
23	d1khca_	 Alignment	not modelled	12.7	20	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: PWWP domain
24	c4n4hA_	 Alignment	not modelled	12.6	26	PDB header: transcription Chain: A; PDB Molecule: zinc finger mynd domain-containing protein 11; PDBTitle: crystal structure of the bromo-pwpp of the mouse zinc finger mynd-type2 containing 11 isoform alpha in complex with histone h3.1k36me3
25	c5xb6D_	 Alignment	not modelled	12.2	20	PDB header: hydrolase Chain: D; PDB Molecule: uncharacterized protein ycyj; PDBTitle: crystal structure of ycyj from e. coli
26	c3pfsA_	 Alignment	not modelled	12.0	11	PDB header: protein binding Chain: A; PDB Molecule: bromodomain and phd finger-containing protein 3; PDBTitle: pwpp domain of human bromodomain and phd finger-containing protein 3
27	c5vc8B_	 Alignment	not modelled	11.9	11	PDB header: dna binding protein Chain: B; PDB Molecule: histone-lysine n-methyltransferase nsd2; PDBTitle: crystal structure of the whsc1 pwpp1 domain
28	c2nfuA_	 Alignment	not modelled	11.0	19	PDB header: dna binding protein Chain: A; PDB Molecule: dna mismatch repair protein msh6;

28	c2g1uA_	Alignment	not modelled	11.0	19	PDBTitle: nmr solution structure of the pwwp domain of mismatch2 repair protein hmsH6 PDB header: structural genomics, unknown function
29	c3c19A_	Alignment	not modelled	10.9	21	Chain: A: PDB Molecule: uncharacterized protein mk0293; PDBTitle: crystal structure of protein mk0293 from methanopyrus kandleri av19
30	c6bwqB_	Alignment	not modelled	10.6	21	PDB header: metal binding protein Chain: B: PDB Molecule: pyridinium-3,5-bisthiocarboxylic acid mononucleotide nickel PDBTitle: larc2, the c-terminal domain of a cyclometallase involved in the synthesis of the npn cofactor of lactate racemase, in complex with3 mnctp
31	d2nlua1	Alignment	not modelled	10.0	8	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: PWWP domain
32	c2jysA_	Alignment	not modelled	9.1	19	PDB header: hydrolase Chain: A: PDB Molecule: protease/reverse transcriptase; PDBTitle: solution structure of simian foamy virus (mac) protease
33	d1bdsa_	Alignment	not modelled	8.1	50	Fold: Defensin-like Superfamily: Defensin-like Family: Defensin
34	c1bdsA_	Alignment	not modelled	8.1	50	PDB header: anti-hypertensive, anti-viral protein Chain: A: PDB Molecule: bds-i; PDBTitle: determination of the three-dimensional solution structure of the anti-hypertensive and antiviral protein bds-i from the sea anemone <i>Metridium senhousii</i> . a study using nuclear magnetic resonance and hybrid distance geometry-dynamical simulated annealing
35	c3c6dB_	Alignment	not modelled	8.1	14	PDB header: virus Chain: B: PDB Molecule: polyprotein; PDBTitle: the pseudo-atomic structure of dengue immature virus
36	d1b12a_	Alignment	not modelled	8.0	18	Fold: LexA/Signal peptidase Superfamily: LexA/Signal peptidase Family: Type 1 signal peptidase
37	c2of3A_	Alignment	not modelled	7.4	13	PDB header: structural protein, cell cycle Chain: A: PDB Molecule: zyg-9; PDBTitle: tog domain structure from <i>C. elegans</i> zyg9
38	c3lyiA_	Alignment	not modelled	6.8	11	PDB header: transcription Chain: A: PDB Molecule: bromodomain-containing protein 1; PDBTitle: pwwp domain of human bromodomain-containing protein 1
39	d1okja2	Alignment	not modelled	6.7	50	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: YeaZ-like
40	c4fu6A_	Alignment	not modelled	6.7	15	PDB header: transcription Chain: A: PDB Molecule: pc4 and sfrs1-interacting protein; PDBTitle: crystal structure of the psp1 pwwp domain
41	c2x35A_	Alignment	not modelled	6.6	6	PDB header: transcription Chain: A: PDB Molecule: peregrin; PDBTitle: molecular basis of histone h3k36me3 recognition by the pwwp domain of2 brpf1.
42	c1uzgA_	Alignment	not modelled	6.1	14	PDB header: viral protein Chain: A: PDB Molecule: major envelope protein e; PDBTitle: crystal structure of the dengue type 3 virus envelope2 protein
43	c5v1eA_	Alignment	not modelled	6.0	39	PDB header: antimicrobial protein Chain: A: PDB Molecule: guavanin 2; PDBTitle: suboptimization of a glycine rich peptide allows the combinatorial space exploration for designing novel antimicrobial peptides
44	c3kopB_	Alignment	not modelled	5.8	25	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein with a cyclophilin-like fold2 (yp_831253.1) from arthrobacter sp. fb24 at 1.90 a resolution
45	c3kksB_	Alignment	not modelled	5.5	9	PDB header: dna binding protein Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of catalytic core domain of biv integrase in crystal form ii
46	c3r9jD_	Alignment	not modelled	5.5	8	PDB header: cell cycle, hydrolase/cell cycle Chain: D: PDB Molecule: cell division topological specificity factor; PDBTitle: 4.3a resolution structure of a mind-mine(i24n) protein complex
47	c3d55A_	Alignment	not modelled	5.5	21	PDB header: toxin inhibitor Chain: A: PDB Molecule: uncharacterized protein rv3357/mt3465; PDBTitle: crystal structure of m. tuberculosis yefm antitoxin
48	d1n27a_	Alignment	not modelled	5.4	10	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: PWWP domain